

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/464,099DATE: 05/19/2000
TIME: 07:33:01

INPUT SET: S35499.raw

#8

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2

3 (1) General Information:

4
5 (i) APPLICANT: Barry, Gerard F.
6 Kishore, Ganesh M.
7 Padgette, Stephen R.
8 Stallings, William C.

9
10 (ii) TITLE OF INVENTION: Glyphosate Tolerant
11 5-Enolpyruvylshikimate-3-Phosphate Synthases

12
13 (iii) NUMBER OF SEQUENCES: 69

14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
17 (B) STREET: 700 Chesterfield Village Parkway
18 (C) CITY: St. Louis
19 (D) STATE: Missouri
20 (E) COUNTRY: USA
21 (F) ZIP: 63198

22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: 09/464,099
31 (B) FILING DATE:
32 (C) CLASSIFICATION:

33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 09/137,440
36 (B) FILING DATE:
37
38 (A) APPLICATION NUMBER: US 08/833,485
39 (B) FILING DATE: 07-APR-1997
40
41 (A) APPLCATION NUMBER: US 08/306,063
42 (B) FILING DATE: 13-SEP-1994

43
44 (vii) PRIOR APPLICATION DATA:
45 (A) APPLICATION NUMBER: US 07/749,611

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/464,099DATE: 05/19/2000
TIME: 07:33:02

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47 (B) FILING DATE: 28-AUG-1991
48
49
50 (vii) PRIOR APPLICATION DATA:
51 (A) APPLICATION NUMBER: US 07/576,537
52 (B) FILING DATE: 31-AUG-1990
53
54
55 (viii) ATTORNEY/AGENT INFORMATION:
56 (A) NAME: Hoerner Jr., Dennis R.
57 (B) REGISTRATION NUMBER: 30,914
58 (C) REFERENCE/DOCKET NUMBER: 38-21(15117)A
59
60 (ix) TELECOMMUNICATION INFORMATION:
61 (A) TELEPHONE: (314) 737-6099
62 (B) TELEFAX: (314) 737-6047
63
64
65 (2) INFORMATION FOR SEQ ID NO:1:
66
67 (i) SEQUENCE CHARACTERISTICS:
68 (A) LENGTH: 597 base pairs
69 (B) TYPE: nucleic acid
70 (C) STRANDEDNESS: double
71 (D) TOPOLOGY: linear
72
73 (ii) MOLECULE TYPE: DNA (genomic)
74
75
76
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
78
79 TCATCAAAAT ATTTAGCAGC ATTCCAGATT GGGTTCAATC AACAAAGGTAC GAGCCATATC 60
80
81 ACTTTATTCA AATTGGTATC GCCAAAACCA AGAAGGAACCT CCCATCCTCA AAGGTTTGTA 120
82
83 AGGAAGAAATT CTCAGTCCAA AGCCTCAACA AGGTCAAGGGT ACAGAGTCTC CAAACCATT 180
84
85 GCCAAAAGCT ACAGGAGATC AATGAAGAAT CTTCAATCAA AGTAAACTAC TGTTCCAGCA 240
86
87 CATGCATCAT GGTCAAGTAAAG TTTCAAGAAAA AGACATCCAC CGAAGACTTA AAGTTAGTGG 300
88
89 GCATCTTGA AAGTAATCTT GTCAACATCG AGCAGCTGGC TTGTGGGGAC CAGACAAAAA 360
90
91 AGGAATGGTG CAGAATTGTT AGGCGCACCT ACCAAAAGCA TCTTGCCTT TATTGCAAAG 420
92
93 ATAAAGCAGA TTCCTCTAGT ACAAGTGGGG AACAAAATAA CGTGGAAAAG AGCTGTCCTG 480
94
95 ACAGCCCAC TACTAATGCG TATGACGAAC GCAGTGACGA CCACAAAAGA ATTCCCTCTA 540
96
97 TATAAGAAGG CATTCAATTCC CATTGAGG ATCATCAGAT ACTAACCAAT ATTTCTC 597
98
99 (2) INFORMATION FOR SEQ ID NO:2:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/464,099DATE: 05/19/2000
TIME: 07:33:03

INPUT SET: S35499.raw

100
 101 (i) SEQUENCE CHARACTERISTICS:
 102 (A) LENGTH: 1982 base pairs
 103 (B) TYPE: nucleic acid
 104 (C) STRANDEDNESS: double
 105 (D) TOPOLOGY: linear
 106
 107 (ii) MOLECULE TYPE: DNA (genomic)
 108
 109
 110 (ix) FEATURE:
 111 (A) NAME/KEY: CDS
 112 (B) LOCATION: 62..1426
 113
 114
 115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 116
 117 AAGCCCGCGT TCTCTCCGGC GCTCCGCCCG GAGAGCCGTG GATAGATTAA GGAAGACGCC 60
 118
 119 C ATG TCG CAC GGT GCA AGC AGC CGG CCC GCA ACC GCC CGC AAA TCC 106
 120 Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser
 121 1 5 10 15
 122
 123 TCT GGC CTT TCC GGA ACC GTC CGC ATT CCC GGC GAC AAG TCG ATC TCC 154
 124 Ser Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser
 125 20 25 30
 126
 127 CAC CGG TCC TTC ATG TTC GGC GGT CTC GCG AGC GGT GAA ACG CGC ATC 202
 128 His Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile
 129 35 40 45
 130
 131 ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC AAT ACG GGC AAG GCC ATG 250
 132 Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met
 133 50 55 60
 134
 135 CAG GCC ATG GGC GCC AGG ATC CGT AAG GAA GGC GAC ACC TGG ATC ATC 298
 136 Gln Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile
 137 65 70 75
 138
 139 GAT GGC GTC GGC AAT GGC GGC CTC CTG GCG CCT GAG GCG CCG CTC GAT 346
 140 Asp Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp
 141 80 85 90 95
 142
 143 TTC GGC AAT GCC GCC ACG GGC TGC CGC CTG ACC ATG GGC CTC GTC GGG 394
 144 Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly
 145 100 105 110
 146
 147 GTC TAC GAT TTC GAC AGC ACC TTC ATC GGC GAC GCC TCG CTC ACA AAG 442
 148 Val Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys
 149 115 120 125
 150
 151 CGC CCG ATG GGC CGC GTG TTG AAC CCG CTG CGC GAA ATG GGC GTG CAG 490
 152 Arg Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/464,099DATE: 05/19/2000
TIME: 07:33:04

INPUT SET: S35499.raw

153	130	135	140	
154				
155	GTG AAA TCG GAA GAC GGT GAC CGT CTT CCC GTT ACC TTG CGC GGG CCG			538
156	Val Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro			
157	145	150	155	
158				
159	AAG ACG CCG ACG CCG ATC ACC TAC CGC GTG CCG ATG GCC TCC GCA CAG			586
160	Lys Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln			
161	160	165	170	175
162				
163	GTG AAG TCC GCC GTG CTG CTC GCC GGC CTC AAC ACG CCC GGC ATC ACG			634
164	Val Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr			
165	180	185	190	
166				
167	ACG GTC ATC GAG CCG ATC ATG ACG CGC GAT CAT ACG GAA AAG ATG CTG			682
168	Thr Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu			
169	195	200	205	
170				
171	CAG GGC TTT GGC GCC AAC CTT ACC GTC GAG ACG GAT GCG GAC GGC GTG			730
172	Gln Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val			
173	210	215	220	
174				
175	CGC ACC ATC CGC CTG GAA GGC CGC GGC AAG CTC ACC GGC CAA GTC ATC			778
176	Arg Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile			
177	225	230	235	
178				
179	GAC GTG CCG GGC GAC CCG TCC TCG ACG GCC TTC CCG CTG GTT GCG GCC			826
180	Asp Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala			
181	240	245	250	255
182				
183	CTG CTT GTT CCG GGC TCC GAC GTC ACC ATC CTC AAC GTG CTG ATG AAC			874
184	Leu Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn			
185	260	265	270	
186				
187	CCC ACC CGC ACC GGC CTC ATC CTG ACG CTG CAG GAA ATG GGC GCC GAC			922
188	Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp			
189	275	280	285	
190				
191	ATC GAA GTC ATC AAC CCG CGC CTT GCC GGC GAA GAC GTG GCG GAC			970
192	Ile Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp			
193	290	295	300	
194				
195	CTG CGC GTT CGC TCC TCC ACG CTG AAG GGC GTC ACG GTG CCG GAA GAC			1018
196	Leu Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp			
197	305	310	315	
198				
199	CGC GCG CCT TCG ATG ATC GAC GAA TAT CCG ATT CTC GCT GTC GCC GCC			1066
200	Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala			
201	320	325	330	335
202				
203	GCC TTC GCG GAA GGG GCG ACC GTG ATG AAC GGT CTG GAA GAA CTC CGC			1114
204	Ala Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg			
205	340	345	350	

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/464,099DATE: 05/19/2000
TIME: 07:33:05

INPUT SET: S35499.raw

206	GTC AAG GAA AGC GAC CGC CTC TCG GCC GTC GCC AAT GGC CTC AAG CTC	1162
207	Val Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu	
208	355 360 365	
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210		
211	AAT GGC GTG GAT TGC GAT GAG GGC GAG ACG TCG CTC GTC GTG CGC GGC	1210
212	Asn Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly	
213	370 375 380	
214		
215	CGC CCT GAC GGC AAG GGG CTC GGC AAC GCC TCG GGC GCC GCC GTC GCC	1258
216	Arg Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala	
217	385 390 395	
218		
219	ACC CAT CTC GAT CAC CGC ATC GCC ATG AGC TTC CTC GTC ATG GGC CTC	1306
220	Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu	
221	400 405 410 415	
222		
223	GTG TCG GAA AAC CCT GTC ACG GTG GAC GAT GCC ACG ATG ATC GCC ACG	1354
224	Val Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr	
225	420 425 430	
226		
227	AGC TTC CCG GAG TTC ATG GAC CTG ATG GCC GGG CTG GGC GCG AAG ATC	1402
228	Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile	
229	435 440 445	
230		
231	GAA CTC TCC GAT ACG AAG GCT GCC TGATGACCTT CACAATGCC ATCGATGGTC	1456
232	Glu Leu Ser Asp Thr Lys Ala Ala	
233	450 455	
234		
235	CCGCTCGGGC CGGCAAGGGG ACGCTCTCGC GCCGTATCGC GGAGGTCTAT GGCTTCATC	1516
236		
237	ATCTCGATAC GGGCCTGACC TATCGCGCCA CGGCCAAAGC GCTGCTCGAT CGCGGCCTGT	1576
238		
239	CGCTTGATGA CGAGGCGGTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGGCTCG	1636
240		
241	ACCGGTCGGT GCTGTCGGCC CATGCCATCG GCGAGGCGGC TTCGAAGATC GCGGTCATGC	1696
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243	CCTCGGTGCG CGGGCGCTG GTCGAGGCGC AGCGCAGCTT TGCAGCGCGT GAGCCGGCA	1756
244		
245	CGGTGCTGGA TGGACGCGAT ATCGGCACGG TGGTCTGCC GGATGCGCCG GTGAAGCTCT	1816
246		
247	ATGTCACCGC GTCACCGGAA GTGCGCGCA AACGCCGCTA TGACGAAATC CTCGGCAATG	1876
248		
249	GCGGGTTGGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGGACA	1936
250		
251	TGGGTCGGGC GGACAGTCCT TTGAAGCCCG CCGACGATGC GCACCTT	1982
252		
253		
254	(2) INFORMATION FOR SEQ ID NO:3:	
255		
256	(i) SEQUENCE CHARACTERISTICS:	
257	(A) LENGTH: 455 amino acids	
258	(B) TYPE: amino acid	

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/09/464,099**

DATE: 05/19/2000
TIME: 07:33:06

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